

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/562,389
Source: IFWP
Date Processed by STIC: 01/11/2007

ENTERED



IFWP

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/562,389

DATE: 01/11/2007

TIME: 09:42:42

Input Set : A:\13407-039US1.txt

Output Set: N:\CRF4\01112007\J562389.raw

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4 <110> APPLICANT: Geesaman, Bard J.
5   Brass, Laura
7 <120> TITLE OF INVENTION: SIRT1 AND GENETIC DISORDERS
10 <130> FILE REFERENCE: 13407-039US1
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/562,389
C--> 12 <141> CURRENT FILING DATE: 2005-12-27
12 <150> PRIOR APPLICATION NUMBER: PCT/US2004/021189
13 <151> PRIOR FILING DATE: 2004-07-01
15 <150> PRIOR APPLICATION NUMBER: US 60/484,327
16 <151> PRIOR FILING DATE: 2003-07-02
18 <160> NUMBER OF SEQ ID NOS: 3
20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 4107
24 <212> TYPE: DNA
25 <213> ORGANISM: Homo Sapiens
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (54)...(2297)
31 <400> SEQUENCE: 1
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34                                     1
36 gcg gac gag gcg gcc ctc gcc ctt cag ccc ggc ggc tcc ccc tcg gcg          104
37 Ala Asp Glu Ala Ala Leu Ala Leu Gln Pro Gly Gly Ser Pro Ser Ala
38           5                      10                      15
40 gcg ggg gcc gac agg gag gcc gcg tcg tcc ccc gcc ggg gag ccg ctc          152
41 Ala Gly Ala Asp Arg Glu Ala Ala Ser Ser Pro Ala Gly Glu Pro Leu
42           20                      25                      30
44 cgc aag agg ccg cgg aga gat ggt ccc ggc ctc gag cgg agc ccg ggc          200
45 Arg Lys Arg Pro Arg Arg Asp Gly Pro Gly Leu Glu Arg Ser Pro Gly
46           35                      40                      45
48 gag ccc ggt ggg gcg gcc cca gag cgt gag gtg ccg gcg gcg gcc agg          248
49 Glu Pro Gly Gly Ala Ala Pro Glu Arg Glu Val Pro Ala Ala Ala Arg
50   50                      55                      60                      65
52 ggc tgc ccg ggt gcg gcg gcg gcg gcg ctg tgg cgg gag gcg gag gca          296
53 Gly Cys Pro Gly Ala Ala Ala Ala Leu Trp Arg Glu Ala Glu Ala
54           70                      75                      80
56 gag gcg gcg gcg gca ggc ggg gag caa gag gcc cag gcg act gcg gcg          344
57 Glu Ala Ala Ala Ala Gly Gly Glu Gln Glu Ala Gln Ala Thr Ala Ala
58           85                      90                      95
60 gct ggg gaa gga gac aat ggg ccg ggc ctg cag ggc cca tct cgg gag          392
61 Ala Gly Glu Gly Asp Asn Gly Pro Gly Leu Gln Gly Pro Ser Arg Glu

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62          100          105          110
64 cca ccg ctg gcc gac aac ttg tac gac gaa gac gac gac gag ggc      440
65 Pro Pro Leu Ala Asp Asn Leu Tyr Asp Glu Asp Asp Asp Asp Glu Gly
66          115          120          125
68 gag gag gag gaa gag gcg gcg gcg gcg gcg att ggg tac cga gat aac      488
69 Glu Glu Glu Glu Glu Ala Ala Ala Ala Ala Ile Gly Tyr Arg Asp Asn
70 130          135          140          145
72 ctt ctg ttc ggt gat gaa att atc act aat ggt ttt cat tcc tgt gaa      536
73 Leu Leu Phe Gly Asp Glu Ile Ile Thr Asn Gly Phe His Ser Cys Glu
74          150          155          160
76 agt gat gag gag gat aga gcc tca cat gca agc tct agt gac tgg act      584
77 Ser Asp Glu Glu Asp Arg Ala Ser His Ala Ser Ser Ser Asp Trp Thr
78          165          170          175
80 cca agg cca cgg ata ggt cca tat act ttg gtt cag caa cat ctt atg      632
81 Pro Arg Pro Arg Ile Gly Pro Tyr Thr Phe Val Gln Gln His Leu Met
82          180          185          190
84 att ggc aca gat cct cga aca att ctt aaa gat tta ttg ccg gaa aca      680
85 Ile Gly Thr Asp Pro Arg Thr Ile Leu Lys Asp Leu Leu Pro Glu Thr
86          195          200          205
88 ata cct cca cct gag ttg gat gat atg aca ctg tgg cag att gtt att      728
89 Ile Pro Pro Pro Glu Leu Asp Asp Met Thr Leu Trp Gln Ile Val Ile
90 210          215          220          225
92 aat atc ctt tca gaa cca cca aaa agg aaa aaa aga aaa gat att aat      776
93 Asn Ile Leu Ser Glu Pro Pro Lys Arg Lys Lys Arg Lys Asp Ile Asn
94          230          235          240
96 aca att gaa gat gct gtg aaa tta ctg caa gag tgc aaa aaa att ata      824
97 Thr Ile Glu Asp Ala Val Lys Leu Leu Gln Glu Cys Lys Lys Ile Ile
98          245          250          255
100 gtt cta act gga gct ggg gtg tct gtt tca tgt gga ata cct gac ttc      872
101 Val Leu Thr Gly Ala Gly Val Ser Val Ser Cys Gly Ile Pro Asp Phe
102          260          265          270
104 agg tca agg gat ggt att tat gct cgc ctt gct gta gac ttc cca gat      920
105 Arg Ser Arg Asp Gly Ile Tyr Ala Arg Leu Ala Val Asp Phe Pro Asp
106          275          280          285
108 ctt cca gat cct caa gcg atg ttt gat att gaa tat ttc aga aaa gat      968
109 Leu Pro Asp Pro Gln Ala Met Phe Asp Ile Glu Tyr Phe Arg Lys Asp
110 290          295          300          305
112 cca aga cca ttc ttc aag ttt gca aag gaa ata tat cct gga caa ttc      1016
113 Pro Arg Pro Phe Phe Lys Phe Ala Lys Glu Ile Tyr Pro Gly Gln Phe
114          310          315          320
116 cag cca tct ctc tgt cac aaa ttc ata gcc ttg tca gat aag gaa gga      1064
117 Gln Pro Ser Leu Cys His Lys Phe Ile Ala Leu Ser Asp Lys Glu Gly
118          325          330          335
120 aaa cta ctt cgc aac tat acc cag aac ata gac acg ctg gaa cag gtt      1112
121 Lys Leu Leu Arg Asn Tyr Thr Gln Asn Ile Asp Thr Leu Glu Gln Val
122          340          345          350
124 gcg gga atc caa agg ata att cag tgt cat ggt tcc ttt gca aca gca      1160
125 Ala Gly Ile Gln Arg Ile Ile Gln Cys His Gly Ser Phe Ala Thr Ala
126          355          360          365

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128	tct	tgc	ctg	att	tgt	aaa	tac	aaa	gtt	gac	tgt	gaa	gct	gta	cga	gga	1208
129	Ser	Cys	Leu	Ile	Cys	Lys	Tyr	Lys	Val	Asp	Cys	Glu	Ala	Val	Arg	Gly	
130	370					375					380					385	
132	gat	att	ttt	aat	cag	gta	gtt	cct	cga	tgt	cct	agg	tgc	cca	gct	gat	1256
133	Asp	Ile	Phe	Asn	Gln	Val	Val	Pro	Arg	Cys	Pro	Arg	Cys	Pro	Ala	Asp	
134				390						395					400		
136	gaa	ccg	ctt	gct	atc	atg	aaa	cca	gag	att	gtg	ttt	ttt	ggg	gaa	aat	1304
137	Glu	Pro	Leu	Ala	Ile	Met	Lys	Pro	Glu	Ile	Val	Phe	Phe	Gly	Glu	Asn	
138			405						410					415			
140	tta	cca	gaa	cag	ttt	cat	aga	gcc	atg	aag	tat	gac	aaa	gat	gaa	gtt	1352
141	Leu	Pro	Glu	Gln	Phe	His	Arg	Ala	Met	Lys	Tyr	Asp	Lys	Asp	Glu	Val	
142			420					425					430				
144	gac	ctc	ctc	att	gtt	att	ggg	tct	tcc	ctc	aaa	gta	aga	cca	gta	gca	1400
145	Asp	Leu	Leu	Ile	Val	Ile	Gly	Ser	Ser	Leu	Lys	Val	Arg	Pro	Val	Ala	
146		435					440					445					
148	cta	att	cca	agt	tcc	ata	ccc	cat	gaa	gtg	cct	cag	ata	tta	att	aat	1448
149	Leu	Ile	Pro	Ser	Ser	Ile	Pro	His	Glu	Val	Pro	Gln	Ile	Leu	Ile	Asn	
150	450					455				460					465		
152	aga	gaa	cct	ttg	cct	cat	ctg	cat	ttt	gat	gta	gag	ctt	ctt	gga	gac	1496
153	Arg	Glu	Pro	Leu	Pro	His	Leu	His	Phe	Asp	Val	Glu	Leu	Leu	Gly	Asp	
154			470						475					480			
156	tgt	gat	gtc	ata	att	aat	gaa	ttg	tgt	cat	agg	tta	ggg	ggg	gaa	tat	1544
157	Cys	Asp	Val	Ile	Ile	Asn	Glu	Leu	Cys	His	Arg	Leu	Gly	Gly	Glu	Tyr	
158			485					490					495				
160	gcc	aaa	ctt	tgc	tgt	aac	cct	gta	aag	ctt	tca	gaa	att	act	gaa	aaa	1592
161	Ala	Lys	Leu	Cys	Cys	Asn	Pro	Val	Lys	Leu	Ser	Glu	Ile	Thr	Glu	Lys	
162			500					505					510				
164	cct	cca	cga	aca	caa	aaa	gaa	ttg	gct	tat	ttg	tca	gag	ttg	cca	ccc	1640
165	Pro	Pro	Arg	Thr	Gln	Lys	Glu	Leu	Ala	Tyr	Leu	Ser	Glu	Leu	Pro	Pro	
166		515				520					525						
168	aca	cct	ctt	cat	gtt	tca	gaa	gac	tca	agt	tca	cca	gaa	aga	act	tca	1688
169	Thr	Pro	Leu	His	Val	Ser	Glu	Asp	Ser	Ser	Ser	Pro	Glu	Arg	Thr	Ser	
170	530					535				540					545		
172	cca	cca	gat	tct	tca	gtg	att	gtc	aca	ctt	tta	gac	caa	gca	gct	aag	1736
173	Pro	Pro	Asp	Ser	Ser	Val	Ile	Val	Thr	Leu	Leu	Asp	Gln	Ala	Ala	Lys	
174				550					555					560			
176	agt	aat	gat	gat	tta	gat	gtg	tct	gaa	tca	aaa	ggg	tgt	atg	gaa	gaa	1784
177	Ser	Asn	Asp	Asp	Leu	Asp	Val	Ser	Glu	Ser	Lys	Gly	Cys	Met	Glu	Glu	
178			565					570					575				
180	aaa	cca	cag	gaa	gta	caa	act	tct	agg	aat	gtt	gaa	agt	att	gct	gaa	1832
181	Lys	Pro	Gln	Glu	Val	Gln	Thr	Ser	Arg	Asn	Val	Glu	Ser	Ile	Ala	Glu	
182			580					585					590				
184	cag	atg	gaa	aat	ccg	gat	ttg	aag	aat	gtt	ggg	tct	agt	act	ggg	gag	1880
185	Gln	Met	Glu	Asn	Pro	Asp	Leu	Lys	Asn	Val	Gly	Ser	Ser	Thr	Gly	Glu	
186		595				600					605						
188	aaa	aat	gaa	aga	act	tca	gtg	gct	gga	aca	gtg	aga	aaa	tgc	tgg	cct	1928
189	Lys	Asn	Glu	Arg	Thr	Ser	Val	Ala	Gly	Thr	Val	Arg	Lys	Cys	Trp	Pro	
190	610					615				620					625		
192	aat	aga	gtg	gca	aag	gag	cag	att	agt	agg	cgg	ctt	gat	ggg	aat	cag	1976

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193 Asn Arg Val Ala Lys Glu Gln Ile Ser Arg Arg Leu Asp Gly Asn Gln
194          630          635          640
196 tat ctg ttt ttg cca cca aat cgt tac att ttc cat ggc gct gag gta      2024
197 Tyr Leu Phe Leu Pro Pro Asn Arg Tyr Ile Phe His Gly Ala Glu Val
198          645          650          655
200 tat tca gac tct gaa gat gac gtc tta tcc tct agt tct tgt ggc agt      2072
201 Tyr Ser Asp Ser Glu Asp Asp Val Leu Ser Ser Ser Ser Cys Gly Ser
202          660          665          670
204 aac agt gat agt ggg aca tgc cag agt cca agt tta gaa gaa ccc atg      2120
205 Asn Ser Asp Ser Gly Thr Cys Gln Ser Pro Ser Leu Glu Glu Pro Met
206          675          680          685
208 gag gat gaa agt gaa att gaa gaa ttc tac aat ggc tta gaa gat gag      2168
209 Glu Asp Glu Ser Glu Ile Glu Glu Phe Tyr Asn Gly Leu Glu Asp Glu
210 690          695          700          705
212 cct gat gtt cca gag aga gct gga gga gct gga ttt ggg act gat gga      2216
213 Pro Asp Val Pro Glu Arg Ala Gly Gly Ala Gly Phe Gly Thr Asp Gly
214          710          715          720
216 gat gat caa gag gca att aat gaa gct ata tct gtg aaa cag gaa gta      2264
217 Asp Asp Gln Glu Ala Ile Asn Glu Ala Ile Ser Val Lys Gln Glu Val
218          725          730          735
220 aca gac atg aac tat cca tca aac aaa tca tag tgtaataatt gtgcaggtac      2317
221 Thr Asp Met Asn Tyr Pro Ser Asn Lys Ser *
222          740          745
224 aggaattggt ccaccagcat taggaacttt agcatgtcaa aatgaatggt tacttgtgaa      2377
225 ctcgatagag caaggaaacc agaaagggtgt aatattttata gggttggtaaa atagattggt      2437
226 tttcatggat aatttttaac ttcattatct ctgtacttgt acaaactcaa cactaacttt      2497
227 ttttttttta aaaaaaaaaa ggtactaagt atcttcaatc agctgttggt caagactaac      2557
228 tttcttttaa aggttcaatt gtatgataaa ttcatatgtg tatatataat tttttttggt      2617
229 ttgtctagt agtttcaaca tttttaaagt tttcaaaaag ccatcggaat gttaaattaa      2677
230 tgtaaggga cagctaactt agaccaaaga atgggtatctt cacttttctt tgtaacattg      2737
231 aatggtttga agtactcaaa atctgttacg ctaaactttt gattctttaa cacaattatt      2797
232 tttaaacact ggcattttcc aaaactgtgg cagctaactt tttaaaatct caaatgacat      2857
233 gcagtgtgag tagaaggaag tcaacaatat gtggggagag cactcggttg tctttacttt      2917
234 taaaagtaat acttggtgct aagaatttca ggattattgt atttacgttc aaatgaagat      2977
235 ggcttttgta ctctctgtgg acatgtagta atgtctatat tggctcataa aactaacctg      3037
236 aaaaacaaat aaatgctttg gaaatgtttc agttgcttta gaaacattag tgccctgcctg      3097
237 gatcccccta gttttgaaat atttgccatt gttgtttaaa tacctatcac tgtggtagag      3157
238 cttgcattga tctttccac aagtattaaa ctgccaaaat gtgaatatgc aaagcctttc      3217
239 tgaatctata ataatggtac ttctactggg gagagtgtaa tattttggac tgctgttttc      3277
240 cattaatgag gagagcaaca ggccctgat tatacagttc caaagtaata agatgttaat      3337
241 tgtaattcag ccagaaagta catgtctccc attgggagga tttggtgtta aataccaaac      3397
242 tgctagccct agtattatgg agatgaacat gatgatgtaa cttgtaatag cagaatagtt      3457
243 aatgaatgaa actagttctt ataatttatt tttattttaaa agcttagcct gccttaaaac      3517
244 tagagatcaa ctttctcagc tgcaaaagct tctagtcttt caagaagttc atactttatg      3577
245 aaattgcaca gtaagcattt atttttcaga ccatttttga acatcactcc taaattaata      3637
246 aagtattcct ctgttgcttt agtattttatt acaataaaaa gggtttgaaa tatagctggt      3697
247 cttttatgcat aaacaccca gctaggacca ttactgccag agaaaaaaat cgtattgaat      3757
248 ggccattttc ctacttataa gatgtctcaa tctgaattta tttggctaca ctaaaagaatg      3817
249 cagtatattt agttttccat ttgcatgatg tttgtgtgct atagatgata ttttaaattg      3877

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250 aaaagtttgt ttttaaattat ttttacagtg aagactgttt tcagctcttt ttatattgta 3937
251 catagtcttt tatgtaattt actggcatat gttttgtaga ctgtttaatg actggatatc 3997
252 ttccttcaac ttttgaaata caaaaccagt gttttttact tgtacactgt tttaaagtct 4057
253 attaaaattg tcatttgact tttttctgtt aaaaaaaaaa aaaaaaaaaa 4107
255 <210> SEQ ID NO: 2
256 <211> LENGTH: 747
257 <212> TYPE: PRT
258 <213> ORGANISM: Homo Sapiens
260 <400> SEQUENCE: 2
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262 1 5 10 15
263 Ala Ala Gly Ala Asp Arg Glu Ala Ala Ser Ser Pro Ala Gly Glu Pro
264 20 25 30
265 Leu Arg Lys Arg Pro Arg Arg Asp Gly Pro Gly Leu Glu Arg Ser Pro
266 35 40 45
267 Gly Glu Pro Gly Gly Ala Ala Pro Glu Arg Glu Val Pro Ala Ala Ala
268 50 55 60
269 Arg Gly Cys Pro Gly Ala Ala Ala Ala Leu Trp Arg Glu Ala Glu
270 65 70 75 80
271 Ala Glu Ala Ala Ala Ala Gly Gly Glu Gln Glu Ala Gln Ala Thr Ala
272 85 90 95
273 Ala Ala Gly Glu Gly Asp Asn Gly Pro Gly Leu Gln Gly Pro Ser Arg
274 100 105 110
275 Glu Pro Pro Leu Ala Asp Asn Leu Tyr Asp Glu Asp Asp Asp Asp Glu
276 115 120 125
277 Gly Glu Glu Glu Glu Glu Ala Ala Ala Ala Ile Gly Tyr Arg Asp
278 130 135 140
279 Asn Leu Leu Phe Gly Asp Glu Ile Ile Thr Asn Gly Phe His Ser Cys
280 145 150 155 160
281 Glu Ser Asp Glu Glu Asp Arg Ala Ser His Ala Ser Ser Ser Asp Trp
282 165 170 175
283 Thr Pro Arg Pro Arg Ile Gly Pro Tyr Thr Phe Val Gln Gln His Leu
284 180 185 190
285 Met Ile Gly Thr Asp Pro Arg Thr Ile Leu Lys Asp Leu Leu Pro Glu
286 195 200 205
287 Thr Ile Pro Pro Pro Glu Leu Asp Asp Met Thr Leu Trp Gln Ile Val
288 210 215 220
289 Ile Asn Ile Leu Ser Glu Pro Pro Lys Arg Lys Lys Arg Lys Asp Ile
290 225 230 235 240
291 Asn Thr Ile Glu Asp Ala Val Lys Leu Leu Gln Glu Cys Lys Lys Ile
292 245 250 255
293 Ile Val Leu Thr Gly Ala Gly Val Ser Val Ser Cys Gly Ile Pro Asp
294 260 265 270
295 Phe Arg Ser Arg Asp Gly Ile Tyr Ala Arg Leu Ala Val Asp Phe Pro
296 275 280 285
297 Asp Leu Pro Asp Pro Gln Ala Met Phe Asp Ile Glu Tyr Phe Arg Lys
298 290 295 300
299 Asp Pro Arg Pro Phe Phe Lys Phe Ala Lys Glu Ile Tyr Pro Gly Gln
300 305 310 315 320

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VERIFICATION SUMMARY

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Input Set : A:\13407-039US1.txt

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date